

```

# from Ito and Houston (2004)
Calculate_Hepatic_Clearance <- function(CLint,fub,Qh=20.7,CLint.scaling =
110,Dn=0.17,density=1.05,model="well-stirred")
{
  if (!(model %in% c("well-stirred", "parallel tube", "dispersion")))
    stop("Model other than \"well-stirred,\" \"parallel tube,\" or \"dispersion\" specified.")

  # Convert from uL/min/10^6 cells to uL/min/g liver
  CLint <- CLint*CLint.scaling

  if (model == "well-stirred")
    CLh <- Qh*fub*CLint/(Qh+fub*CLint)
  else if (model == "parallel tube")
    CLh <- Qh*(1-exp(-fub*CLint/Qh))
  else if (model == "dispersion")
  {
    Rn <- fub*CLint/Qh
    a <- sqrt(1 + 4*Rn*Dn)
    CLh <- Qh*(1 - 4*a/((1+a)^2*exp((a-1)/2/Dn)-(1-a)^2*exp(-(a+1)/2/Dn)))
  }

  return(CLh)
}

```